

## REPLACEMENT SHEET

><MW: 120922

MVFPMTLKRQILILFNIILISKLLGARWFPKTLPCDVLDVPKNHVIVDCTDKHLTEIP  
GGIPTNTTNLTLTINHIPDISPASFHRLDHVEIDFRCNCVPIPLGSKNNMCIKRLQIKP  
RSFSGLTYLKSLYLDGNQLLEIPQGLPPSLQLLSLEANNIFSIRKENTELANEIILYLG  
QNCYYRNPCYVSYSIEKDAFLNLTKLKVSLKDNNVTAVPTVLPSTLTELYLYNNMIAKI  
QEDDFNNLNQLQILDLSGNCPRCYNAPFFCAPCKNSPLQIPVNADALTELKVLRLHSN  
SLQHVPPRFKNINKLQELDLSQNFLAKEIGDAKFLHFLPSLIQLDLSFNFELQVYRASM  
NLSQAFSSLKSLKILRIRGYVFKEKSFNLSPLHNLQNLEVLDLGTNFIKIANLSMFQF  
KRLKVIDLSVNKISPSGDSSEVGFCNARTSVESYEPPQVLEQLHYFRYDKYARSCRFKNK  
EASFMSVNESCYKGQTLDLSKNSIFFVKSSDFQHLSFLKCLNLSGNLISQTLNGSEFQP  
LAELRYLDFSNRLLHSTAFEELHKLEVLDISSNSHYFQSEGITHMLNFTKNLKVLQK  
LMMNDNDISSLRTMESESRLTLEFRGNHLDVLWREGDNRYLQLFKNLLKLEELDISKN  
SLSFLPSGVFDGMPPNLKNLSSLAKNGLKSFSWKKLQCLKNLETLDLSHNQLTTVPERLSN  
CSRSLKNLILKNNQIRSLTKYFLQDAFQLRYLDLSSNKIQMIQKTSFPEVNLLKMLL  
HHNRFLCTDAWFVWWNVNHTEVТИPYLATDVTCVGPGAHKGQSVISLDLYTCELDLTNL  
ILFSLSISVSLFLMMMTASHLYFWDVWYIYHFCKAKIKGYQRLISPDCYDAFIVYDTK  
DPAVTEWVLAELVAKLEDPREKHFLCLEERDWLPGQPVLENLSQSICLSKKTVFVMTDK  
YAKTENFKIAFYLSHQRLMDEKVDVIILIFLEKPFQSKFLQLRKRLCGSSVLEWPTNPQ  
AHPYFWQCLKNALATDNHVAYSQVFKETV

**FIG. 1**

# REPLACEMENT SHEET

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><insert starts here>CCCATCTCAAGGCTGATCTGGCACCTCTCATGCTCTGCCTCAACAGACTCTACA
TTCCATTGGAAAGAAAGACTAAAAA
><MET { trans=1-s, dir=f, res=1 } >
ATGGGTGTTCCAATGTGGACACTGAAGAGACAAATTCTTAACTCCTTTAAACATAATCCTTA
ATTCCCAAACCTCCTGGGCTAGATGGTTCCCTAAACTCTGCCCTGTGATGTCACACTCTG
GATGGTCCAAAGAACCATGTGATCGTGGACTGCACAGACAAGCATTGACAGAAATTCCCT
GGAGGTATTCACCGAACACCCGAACCTCACCCCTACCCATTAACCACATACCAGACATC
TCCCCAGGGTCCCTTACAGAGACTGGACCATCTGGTAGAGAGATCGATTCAAGAGGCTGCAGATTAAACCC
GTACCTATCCACTGGGGTCAAAAACACACATGTGATCAAGAGGCTGCAGATTAAACCC
AGAAGCTTIACTGGACTCACTTAAATTCACCTTAAATCCCTTACCTGGATGGAAACCAGCTACTA
GAGATACCGGAGGGCCTCCGGCCTAGCTTACAGGCTCTCAGGCTTGAGGCCAACAAACATC
TTTCCATCAGAAAAGAGAACATCTAACAGGAAACTGGCCAACATAGAAATACTCTACCTGGGC
CAAACACTGTTATTATCGAAATCCTTGTATGTTCAATTCAATAGAGAAAAGATGCCTTC
CTAAACCTGACAAAGTTAAAGTGCTCTCCCTGAAGATAACAAATGTCACAGCCGTCCT
ACTGTTTGGCATCTTACAGAACTTAAACCAATTACAAATTCTGACCTTAAGTGGAAATTGC
CAAGAAGATGATTAAACCTCAACCAATTACAAATTCTGACCTTAAGTGGAAATTGC
CTTCGTTGTTATAATGGCCCCATTTCCTTGTGGCCGGTGTAAATAATTCTCCCTACAG
ATCCCTGTAATGCTTTGATGCGCTGACAGAATTAAAGTTTACGTTACACAGTAAC
TCTCTCAGCATGTGCCCTAACAGATGGTTAAAGAACATCAACAAACTCCAGGAACCTGGAT
CTGTCCTAAACACTCTGGCCAAAGAAATTGGGGATGCTAAATTCTGCATTTCCTCCC
AGCCTCATCCAATTGGACTAACTTTAACCTCTGCCTATTACATAATCTCCTAAATCTGAA
AATCTATCACAAGGATTCTTCACTGAAGCCTGAAATTCTGAGGATCTGAGGATAT
GTCTTAAAGAGTGGAAAGCTTTAACCTCTGCCTAAATGGCTAACTCTGCTTAAACAAATT
GTCCTGATCTGGACTAACTTTAACCTCTGCCTATTACATAATCTCCTAAATCTGAA
AATCTATCACAAGGATTCTTCACTGAAGCCTGAAATTCTGAGGATCTGAGGATCTGAGGAT
GAAATTACATTTCAGATATGATAAGTATGCAAGGAGTTGCAAGTTCAACCTTCAGGAGATCAAGT
GAGGCTTCTTCATGTCGTTAATGAAAGCTGCTACAAGTATGGGCAGACCTGGATCTG
AGTAAAAATAGTATATTGTCAAGTCTCTGATTTCAAGTCTTCTCTCAA

```

**FIG. 2A**

## REPLACEMENT SHEET

TGCCCTGAATCTGTCAGGAAATCTCATTAGCCAAAACCTCTTAATGGCAGTCTTAATTTCCAAACCT  
TTAGCAGAGCTGAGATATTGGACTTCTCCAAACAACCGGCTTGATTACTCCATTCAACA  
GCATTGAAAGAGCTTCACAAAACCTGAAAGTTCTGGATAATAAGCAGTTAACCTTCAATT  
CAATCAGAAGGAATTACTCATATGCTAAACTTACCAAGAACCTAAAGGTCTGCAAGAAA  
CTGATGATGAAACGACAATGACATCTCTCCACCAGCAGCACATGGAGAGTGGAGTGGAGTCT  
CTTAGAAACTCTGGAATTCAAGAGGAATCACTTAGATGTTTATGGAGAGAACGGTGTATAAC  
AGATACTTACAAATTATTCAAGAACATCTGCTAAAGAACATTAGAGAAATTAGACATCTCTAAAGAT  
TCCCTAAGTTCTGGCCTCTGGAGTTTTGATGGTATGCCCTCCAAATCTTAAGAACATTCTC  
TCTTGGCCAATAATGGGCTCAAATCTTCAAGTGGAAAGAACCTCAGTGTCTAAAGAAC  
CTGGAAACACTTGGACCTCAGCCACAACTGACCACACTGTCCTGAGAGATTATCCAAAC  
TGTTCCAGAAGCCTCAAGAACATTCTGATTCTTAAGAATAATCAAAATCAGGAGTCTGACGAAG  
TATTTCCTACAAAGATGCCCTCCAGTTGGCATATCTGGATCTCAGCTCAAATAAATCAG  
ATGATCCAAAAGACCAGCCTCCAGAAAATGCTCCTCAACAAATCTGAAGATGTTGGCTTTAACCAT  
CATCATAAATCGGTTTCTGTCACCTGTGATGCTGTGTTGGGTTAACCAT  
ACGGAGGTGACTATTCCCTAACCTGGCCACAGATGTGACTTGTGACTAACACTG  
AAGGGCCAAGGTGTGATCTCCCTGGATCTGTACACCTGTGAGTTAGATCTGACTAACCTG  
ATTCTGTTCTCACTTCCATATCTGTATCTCTCTTCTCATGGTGTGATGACAGCAAGT  
CACCTCTATTCTGGGATGTTGGTATATTACCATTTCTGTAAGGCCAAGATAAAGGGG  
TATCAGCGCTTAATATCACCAGACTGTTGCTATGATGCTTTTATGTTGATGACACTAA  
GACCCAGCTGTGACCGAGTGGGTTGGCTGAGCTGGCTGAGCTGGCCAAACACTGGAAAGACCCAAAG  
GAGAAACATTAAATTATGTCAGGAAAGGGACTGGTTACCAAGGGCAGGCTG  
GAAAACCTTCCAGAGCATACAGCTTAGCAAAAGACAGTGTGATGACAGACAAAG  
TATGCAAAAGACTGAAATTTAAGATAGCATTACTGTCCCATTAGGGCTCATGGAT  
GAAAAGTTGATGTTGATTATCTTGATATTCTCTGAGAAGGCCCTTCTGAAGGTCCAAAGTTC  
CTCCAGCTCCGGAAAAGGCTCTGIGGGAGTTCTGCTAAAGAACGCGCTGGCCACAGACAATCATGTGGCC  
GCTCACCCATACTCTGGCAGTGTCTAAAGAACGCGCTAGGCCCTTCTTTGGCAAAACACAAACTGGCTAGTT  
TATAGTCAGGGTGTCAAGGAAACGGTCTAGGCCCTTCTTTGGCAAAACACAAACTGGCTAGTT  
TACCAAGGAGGGCCTGGC

**FIG. 2B**

## REPLACEMENT SHEET

MENMFLQSSMLTCIFLLISGSCELCAEENFSRSYPCDEKKQNDSVIAECNSRRLQEVPQT  
VGKYVTELDLSDNFITHITNESFQGLQNLTKINLNHNPNVQHQNGNPGIQSNGLNITDGA  
FLNLKNLRELLLEDNQLPQIPSGLPESITELSSIQNNIYNITKEGISRLINLKNLYLAWN  
CYFNKVCEKTNIEDGVFETLTNLELLSLSFNSLSHVPPKLPSSLRKLFLSNTQIKYISEE  
DFKGLINLTLDDLSGNCPRCFNAPFPCVPCDGGASINIDRFAFQNLTQLRYLNLSSTSRL  
KINAAWFKNMMPHLKVLDLEFNYLVGEIVSGAFLTMLPRLEILDLSFNYIKGSYPQHINIS  
RNFSKLLSLRALHLRGYVFQELREDDFQPLMQLPNLSTINLGINFQKQIDFKLFQNFSNL  
EIIYLSERISPLVKDTRQSYANSSSFQRHIRKRSTDFEFDPHSNFYHFTRPLIKPQCA  
AYGKALDLSSLNSIFFIGPNQFENLPDIACLNLSANSNAQVLSGTEFSAIPHVKYLDLTNN  
RLDFDNASALTELDLEVLDLSYNSHYFRIAGVTHHLEFIQNFNTNLKVNLSHNNIYTLLT  
DKYNLESKSLVELVFSGNRLDILWNDDDRYISIFKGLKNLTRLDSLNRLKHIPNEAFL  
NLPASTELHINDNMLKFFNWTLLQQFPRLELLDLRGNKLLFLTDSSLSDFTSSLRTLLLS  
HNRISHLPSGFLSEVSSLKHLDLSSNLLKTINKSALETKTTKLSMLELHGNPFECTCDI  
GDFRRWMDEHNVKIPRLVDVICASPGDQRGKSIVSLELTTCVSDVTAVILFFFFFIT  
MVMLAALAHHLFYWDVWFIVNVCLAKVKGYRSLSTSQTFYDAYISYDTKDASVTDWVINE  
LRYHLEESRDKNVLLCLEERDWDPGLAIIDNLMQSINQSKKTVFVLTKYAKSWNFKTAF  
YLALQRLMDENMDVIIFILLEPVLQHSQYLRQRICKSSILQWPDNPKAEGLFWQTLRN  
VVLTENDSRYNNMYVDSIKQY

<1041 residues, 0 stop; molecular weight: 119856.26

**FIG. 3**

# REPLACEMENT SHEET

><cDNA starts here>GGGTACCCATTCTGGCTGCTGCAAGTTACGGAATGAAAATTAGAACAGA  
AAC  
><MET { trans=1-s , dir=f , res=1 }>  
ATGGAAAAACATGTTCCCTTCAGTCGTCAATGCTGACCTGCATTTCCTGCTTAATATCTGGT  
TCCTGTGAGTTATGGCAGCGAAGAAAATTCTAGAAGCTATCCTGTGATGAGAAAG  
CAAATGACTCAGTTATGGAGAGTGAGCGAATCGTGGACTACAGGAAGTCCCCAAACG  
GTGGCCAATAATGTTGACAGAACTAGACCTGTGATAATTCTCATCACACACATAACGAAT  
GAATCATTCAAGGGCTGCCAAATCTCACTAAATAATCTAAACCACAAACCCCAATGTA  
CAGCACCAGAACGGAAATCCCGGTATACAATTCAATGGCTTGAAATATCACAGACGGGCA  
TTCCTCAACCTAAAAACCTTAAGGGAGTTACTGCTTGAAAGACAACCGATTACCCCAAATA  
CCCTCTGGTTGCCAGAGTCTTGACAGAACTTAGTCTAAATTCAAACAAATAATACAAC  
ATAACTAAAGAGGGCATTCAAGACTTAAACTTGAAGAAATTCTCTATTGGCCCTGGAAAC  
TGCTATTAAACAAAGTTGCGAGAAAACATAAGAAGATGGAGTATTGAAACGGCTG  
ACAAATTGGAGGTTGCTTACATTCTTCAATTCTTCAACAGTGGCACCCAAACTG  
CCAAGCTCCCTACGCCAAACTTTCTGAGCAACACCCAGATCAAATACATTAGTGAAGAA  
GATTCAAGGGATTGATAAATTAAACATTACTAGATTAAAGGGGAACCTGTCGGAGGTGC  
TTCAATGCCCATTCCTGCGTGCCTTGTGATGGTGGCTTCATTAAATATAGATCGT  
TTGCTTTCAAAACTTGACCCAAACTTCGATAACCTAAACCTCTAGCATTCCCTCAGG  
AAGATTAAATGCTGCCTGGTTAAAATATGGCTCATCTGAAGGGCTGGATCTTGAAATT  
AACTATTAGGGAGAAATAGTCTCTGGGCATTAACTTAAAGGGAGTTATCCACAGCATTAAATT  
ATACCTGACTTGTCTTTAACTTAACTTAAAGGGAGTTATCCACAGCATTAAATT  
AGAAACTTCTAAACTTTGTCTCTAGGGCATTAAAGGGTTATGTGTCCAG  
GAACTCAGAGAACAGATGATTCCAGGCCCTGATGCCAGCTCCAAACTTATCGACTATCAC  
TTGGTATTAAATTAAAGCAAATGATTCAAACCTTTCCAATTCTCCAAATCTG

**FIG. 4A**

## REPLACEMENT SHEET

GAAATTACTTGTCAAGAAAACAGAATAATCACCGTGGTAAAAGATAACCGGGCAGAGT  
TATGCAAATAGTTCCCTCTTTCAACGTCAATACCGGAACGACGCTCAACAGATTTGAG  
TTTGACCCACATTGAAACTTTATCATTCACCCGTCCTTAATAAGCCACAATGTGCT  
GCTTATGGAAAAGCCTTAGATTAGCTAACAGTATTTCATGGCCAAACCAA  
TTGAAAATCTCCCTGACATTGCCGTAAATCTGTCTGCAAAATAGCAATGCTCAAGTG  
TTAAGTGGAACTGAATTTCAGGCCATTCTCATGTCAAAATTTGGATTGACAAACAAAT  
AGACTAGACTTGATAATGCTAGTGCTCTTAACTGAATTTGTCGAAGTCTAGAT  
CTCAGCTATAAATTCAACATTCAACTATTAGCAATAAGCAGGGTAACACATCATCTAGAATTATT  
CAAATTTCACAAATCTAAAAGTTAAACFTGAGCCACAACAAACATTAACTTTAAC  
GATAAGTATAACCTGGAAAGCCAAGTCCCTGGTAGAATTAGTTTCAGTGGCAATGGCCT  
GACATTTTGTGGAATGTGATGACAACAGGTATACTCCCATTTCAAGGCTCAAGAAT  
CTGACACGGTCTGGATTIATCCCTTAATAGGTGAAGGCACATCCCACATTGAAAGCATTCTT  
AATTGGCCAGGGAGTCTACTGAACACTACATAAATGATAATATGTTAAAGTTTTAAC  
TGGACATTACTCCAGCAGTTCTCTCGTCTCGAGTTGACTTACGTGGAAACAAACTA  
CTCTTTTAACTGATAAGCTATCTGACTTACATCTCCCTCGGACACTGCTGCTGAGT  
CATACAGGATTCCACCTACCCCTCTGGCTTCTTCTGAAGTCAGTAGTCAGGCAC  
CTCGATTAAAGTCCAATCTGCTAAACAAATCAACAAATCCGCACTGAAACTGACATT  
ACCACCAAATTATCTATGTTGAACTACAGGAAACCCCTTGAATGCAACTGTCAGATT  
GGAGATTCCGAAGATGGATGGGATGAACATCTGAATGTCAAATTCCAGACTGGTAGAT  
GTCATTGTCAGTCACTGCAGTTGATTTTCACTGGGTCTTCACTGGGTCTGGAGCTAAC  
ACTTGTGTTCAAGTGTCACTGCAGTTGATTTTCACTGGGTCTTCACTGGGTCTGGAGCTAAC  
ATGGTTATGGTGGCTGGCTGCCCCACATTGTTACTGGGATGTTGGTTTATAT  
AATGGTGTGTTAGCTAAGGTAAAAGGCTACAGGTCTCCACATCCCACACTTCTAT  
GATGCTTACATTCTTATGACACCAAGATGCCCTCTGTTACTGACTGGGTGATAAATGAG

**FIG. 4B**

# REPLACEMENT SHEET

Sequence ss . DNA42663

CTGGCCTACCACTTGAGAGAGCCGAGACAAAACGTTCTCCTTGTCTAGGGAGGG  
GATTGGGACCCGGGATTTGCCATCATCGACAACCTCATGCAGGCATCAACCAAGCAAG  
AAAACAGTATTGTTAACAAATAATGCCAAAAGCTGGAAACTTAAACAGCTTT  
TACTGGCTTGAGGGCTAATGGATGAGAACATGGATGTGATTATATTATCCTGCTG  
GAGCCAGTGTACAGGATTCTCAGTATTGGGGCTACGGCAGGGATCTGTAAGAGCTCC  
ATCCCTCAGTGGCTGACAACCCGGAAAGGCAAGGAAGGCTTGTGTTGGCAAACCTCTGAGAAAT  
GTGGCTTGACTGAAAATGATTCAACGTATAACAATATGTATGTCGATTCCATTAAAGCAA  
TACTAACTGACGTTAAGTCATGATTTCGGCCATAATAAAGATGCAAAGGAATGACAATT  
CTGTATTAGTTATCTATGGCTATGTAACAAATTATCCAAAACCTTAGTGGTTAAAAACAA  
CACATTGGCTGGCCACAGTTTGAGGGTCAAGGACTCCAGGCCAGCATAACTGGTCC  
TCTGCTCAGGGTGTCTCAAGGGCTGCAATGTAGGTGTTCAACAGAGACATAGGCATCACT  
GGGGTCAACACTCATGTGTTCTGGATTCAATTCTCTGGCTATTGGCCAAGG  
CTATACTCATGTAAGCCATGGGAGCCTCTCCCACAAGGCAGCTGCTTCATCAGAGCTAG  
CAAAAAGAGGAGGTTGCTAGCAAGATGCAAGTCAAAATCTTTGTAATCGAAATCAAAG  
TGATATCTCATCACTTGGCCATATTCTATTGGTAAAGTAACACAGGTCCCACCA  
CTCCATGGGAGTGCACCACTCAGTCCAGGGAAACAGCTGAAGGCAAGATGGTGAAGCT  
TGATTTGCTTCAGTTGGTCATCAACTATTCCCTTGACTGCTGCTGGATGGCCTGCT  
ATCTTGATGATGATGTTGAAATATCAGGAGGAGGATCACTGGGACCATCTTAGCAGT  
TGACTTAACACATCTTCATATACTAAGAACTTTGCCACTGTGACTAATGGTCC  
AATATTAAGCTGGTGTATTATCATATACTATGTTACATGGCTACATGGTTATATTATGCTG  
TGTTGCGTTGGTTATTACAGTGTGCTTTACAAAATTTGCTGAACATTGACTT  
CTAAGGTTAGATGCCATTAAAGAACTGAGATGGATAGCTTTAACCT  
TTACCATTTAAAGTATGCAAGCTAAATCGAAGCTTGGTCTATTTGTTAATTG  
CATTGCTGTAATCTTAAATGATGAATAAAAATGTTCAATTTCATTAAA  
AAA

**FIG. 4C**

REPLACEMENT SHEET

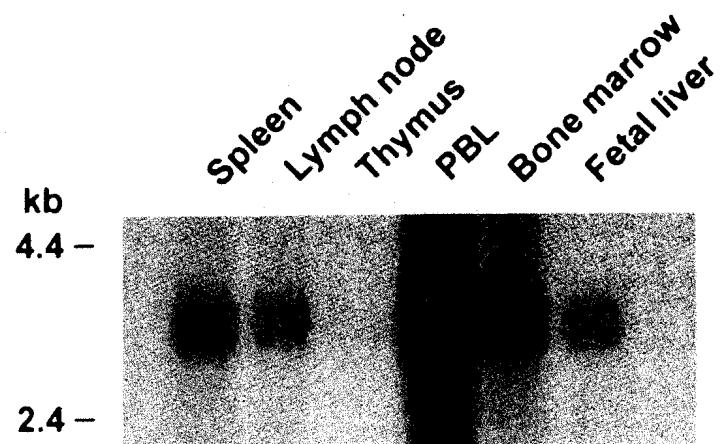


FIG. 5A

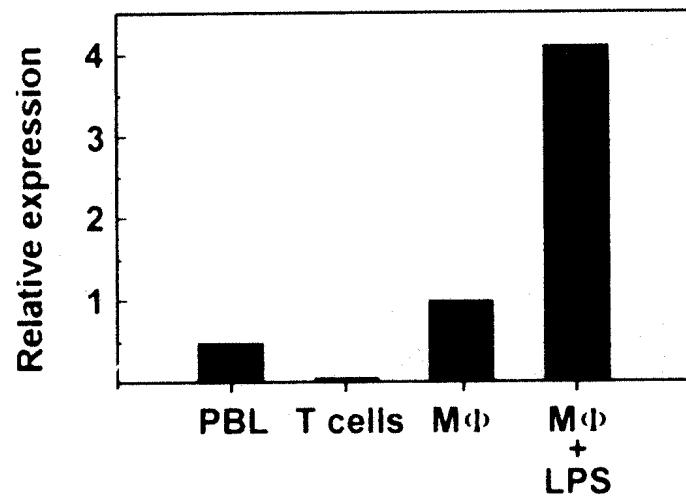


FIG. 5B

REPLACEMENT SHEET

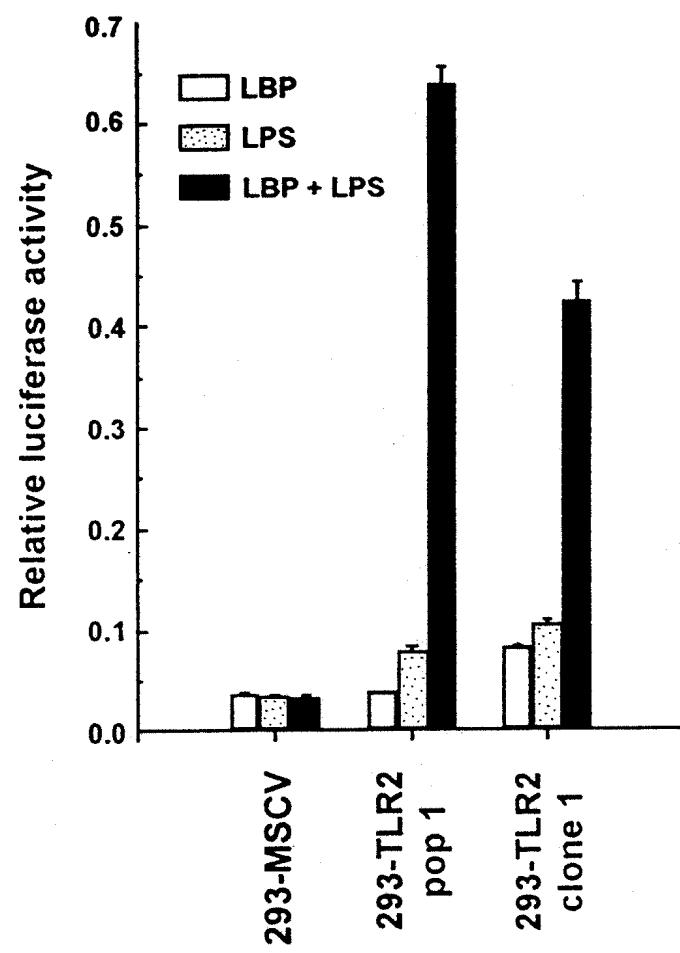


FIG. 6A

REPLACEMENT SHEET

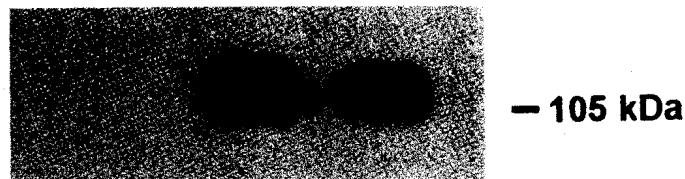


FIG. 6B

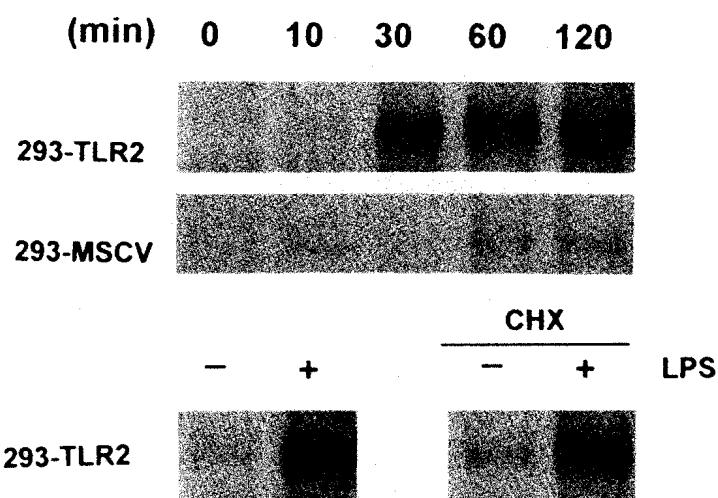


FIG. 6C

REPLACEMENT SHEET

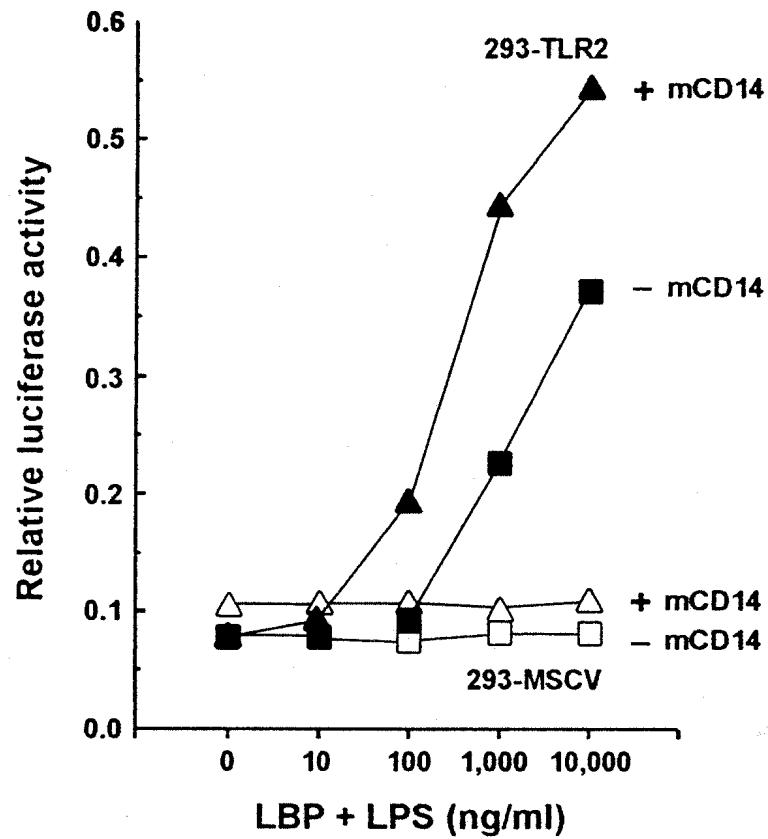


FIG. 6D

REPLACEMENT SHEET

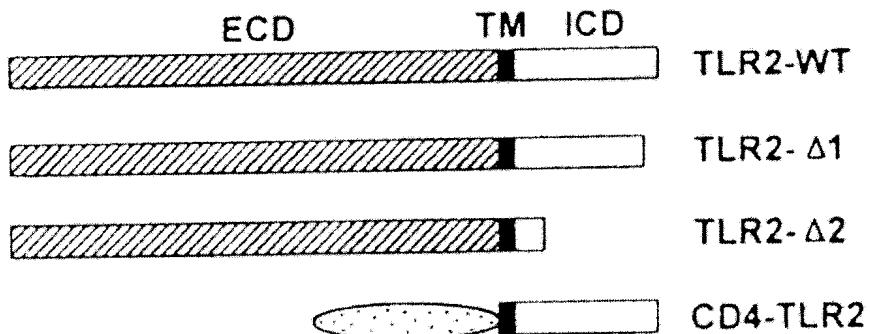


FIG. 7A

IL1-R    SAKTRFWKNVRYHMPV    524  
TLR2    AQREGFWVNLRRAIKS    784  
      : | | | : | : | : |  
      ↓  
TLR2-Δ1

FIG. 7B

REPLACEMENT SHEET

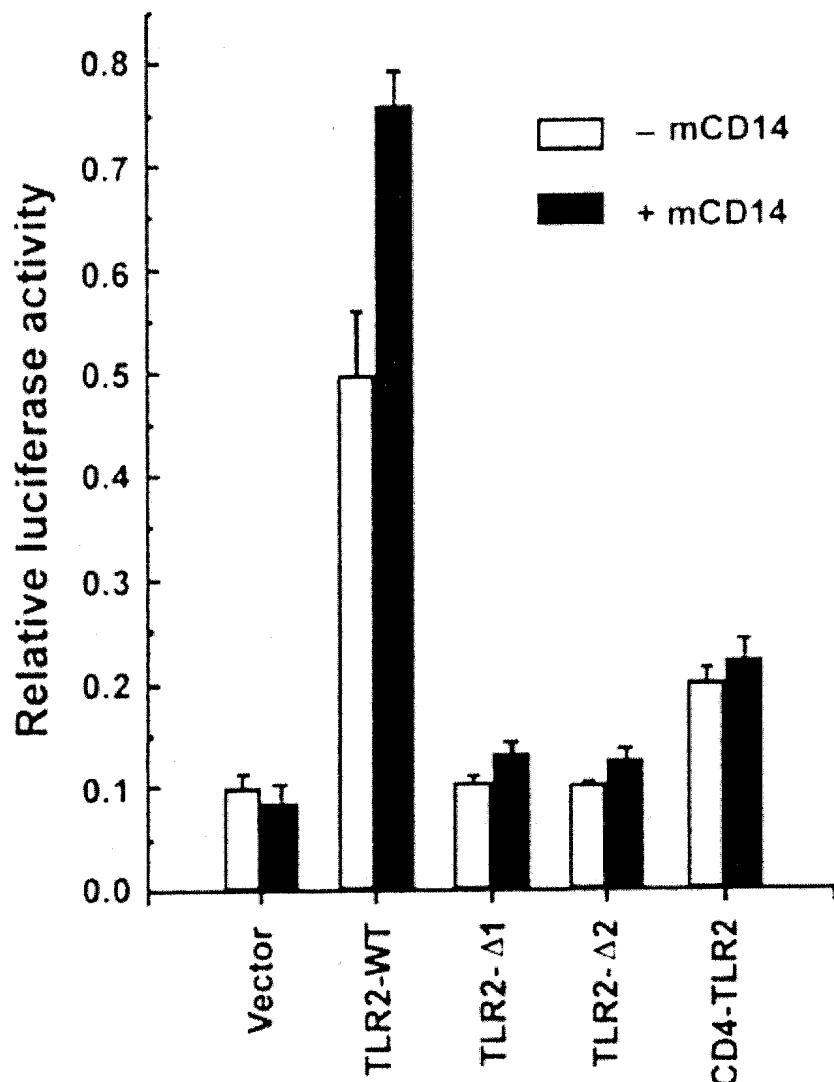


FIG. 7C

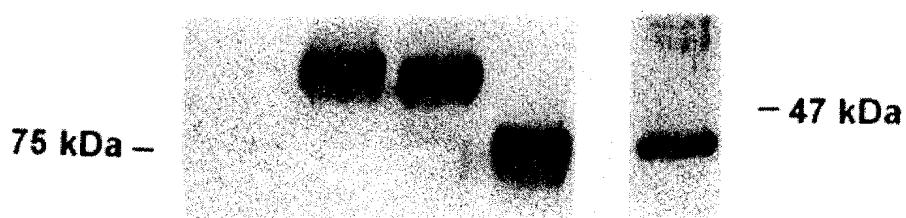


FIG. 7D

REPLACEMENT SHEET

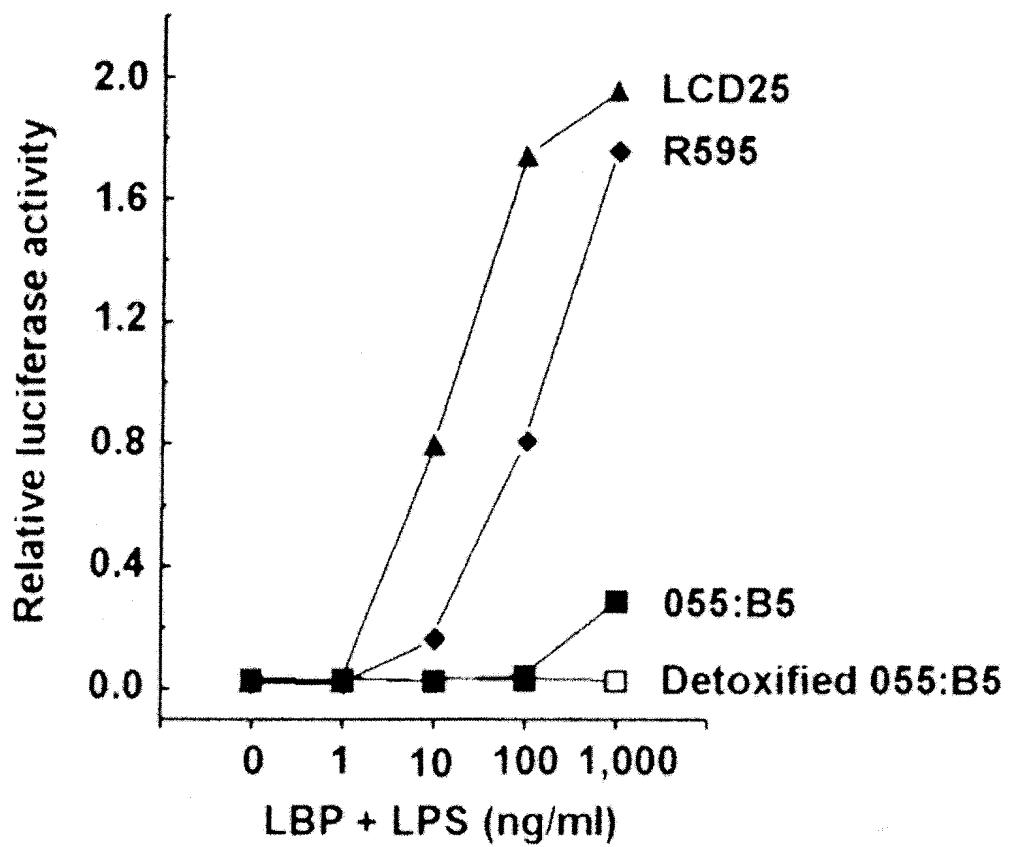


FIG. 8A

REPLACEMENT SHEET

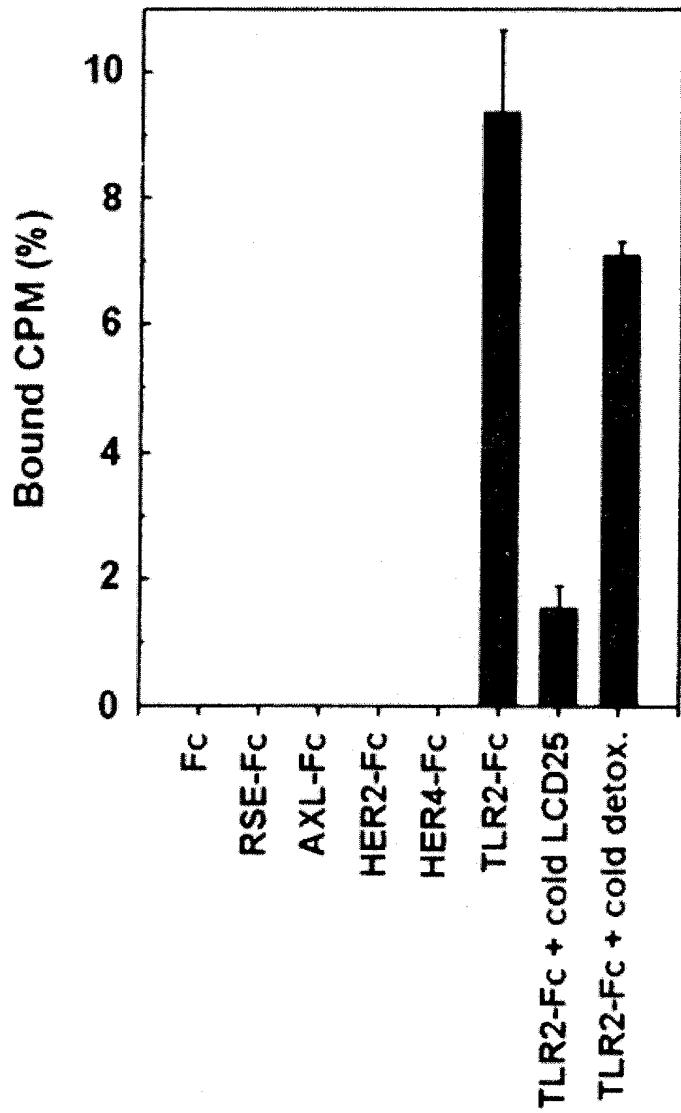


FIG. 8B

## REPLACEMENT SHEET

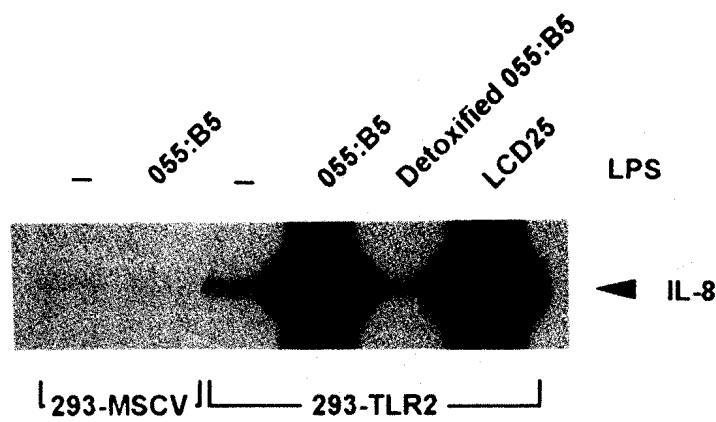


FIG. 9

## REPLACEMENT SHEET

GTTATGCCTAGAAAACATTCTCAAGAATTAGAATTACGATATGCTGTCAAACACAATGA  
CTTATTGAACCTCTTATTGTAGGTGAAGCACTGGACAATGCCACATACTTGTGG  
ATGGTGTGGTCTTGGGGTCATCATCAGCCTCTCCAAGGAAGAACCTCCAATCAGGCT  
TCTCTGTCTGTGACCGCAATGGTATCTGCAAGGGCAGTCAGGATCTTAAACTCCATT  
CCCTCAGGGCTCACAGAAGCTGAAAAAGCCTTGACCTGTCCAACAACAGGATCACCTAC  
ATTAGCAACAGTGACCTACAGAGGTGTGAACCTCCAGGCTCTGGTGCTGACATCCAAT  
GGAATTAAACACAATAGAGGAAGATTCTTTCTCCCTGGGAGTCTTGAACATTTAGAC  
TTATCCTATAATTACTTATCTAATTATCGTCTCCTGGTCAAGCCCCTTCTCTTAA  
ACATTCTAAACTACTGGAAATCCTTACAAAACCTAGGGAAACATCTCTTTCT  
CATCTCACAAAATTGCAAATCCTGAGAGTGGAAATATGGACACCTTCACTAAGATTCAA  
AGAAAAGATTTGCTGGACTTACCTCCTGAGGAACCTGAGATTGATGCTTCAGATCTA  
CAGAGCTATGAGCCAAAAGTTGAAGTCATTAGAATGTAAGTCATCTGATCCTTCAT  
ATGAAGCAGCATATTACTGCTGGAGATTGGTAGATGTTACAAGTCCGTGGAATGT  
TTGGAACTGCGAGATACTGATTGGACACTTCCATTTCAGAACTATCCACTGGTGAA  
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TGTACCCCTTAATGGAGTTGTAATTAGAGCATCTGATAATGACAGAGTTAGATCCA  
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AAAGTTTCTGGTCTTGTACTTCAACATTTAAATCATTAGAATACTTGGAT  
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CCCTCTCACAAACTTAATTAAAGGCAAATCATTGGCATCATTGGAAAAACCGGA  
GAGACTTTGCTCACTGAAAAACTGACTAACATTGATATCAGTAAGAATAGTTTCA  
TCTATGCCTGAAACTGTCAGTGGCCAGAAAAGATGAAATATTGAACCTATCCAGCACA  
CGAATACACAGTGTAAACAGGCTGCATTCCAAGACACTGGAAATTAGATGTTAGCAAC  
AACAACTCTAATTATTCTTGAATTGCCGCAACTCAAAGAAACTTATATTCCAGA  
ATAAGTTGATGACTCTACCAGATGCCCTCTTACCCATGTTACTAGTATTGAAAATC  
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ACTTTGGAAGCTGGTGGCAATAACTCATTGCTCCTGTGAATTCCCTCCTCACTCAG  
GAGCAGCAAGCACTGCCAAGTCTGATTGATTGCCAGCAAATTACCTGTGACTCT  
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AGGACAGCACTGGTGTCTGGCATGTGCTGTCTGTTCTGCTGATCCTGCTCACGGGG  
GTCCTGTGCCACCGTTCCATGGCTGTGGTATATGAAAATGATGTTGGGCTGGCTCCAG  
GCCAAAAGGAAGCCCAGGAAAGCTCCAGCAGGAACATCTGCTATGATGCATTGTTCT  
TACAGTGAGCGGGATGCCACTGGTGGAGAACCTTATGGTCCAGGAGCTGGAGAACCTC  
AATCCCCCTTCAGTTGTCTTCATAAGCGGGACTTCATTGGCAAGTGGATCATT  
GACAATATCATTGACTCCATTGAAAAGAGCCACAAACTGCTTTGTGCTTCTGAAAAC  
TTTGTGAAGAGTGAGTGGTGCAAGTATGAACTGGACTCTCCATTCCGTCTTTGAT  
GAGAACAAATGATGCTGCCATTCTCATTCTGTGGAGCCATTGAGAAAAAGCCATTCCC  
CAGCGCTCTGCAAGCTGCGGAAGATAATGAACACCAAGACACTACCTGGAGTGGCCATG  
GACGAGGCTCAGCGGGAGGATTGGTAAATCTGAGAGCTGCGATAAGTCCTAGGTT  
CCCATATTAAAGACCAGTCTTGTCTAGTTGGATCTTATGTCACTAGTTAGTTAAG  
TTCATTCAAGACATAATTATAAAACTACGTGGATGTACCGTCATTGAGGACTTGCTT  
ACTAAAACATACAAAACCTCAAA

**FIG. 10**

## REPLACEMENT SHEET

MPHTLWMVWVLGVIISLSKEESSNQASLSCDRNGICKGSSGSLN SIPSGLTEAVKSLDL  
SNRITYISNSDLQRCVNLQALVLTSGINTIEEDSFSSLGSLEHLDLSYNLYSNNLSSS  
WFKPLSSLTFLNLLGNPYKTLGETSLFSLTKLQILRVGNMDTFTKIQRKDFAGLTGLE  
ELEIDASDLQSYPEPKSLKSIQNVSHLILHMKQHILLLEIFVDVTSSVECLELRDLDL  
FHFSSELSTGETNSLIKKFTFRNVKITDESLFQVMKLLNQISGLLELFDDCTLNGVGNF  
RASDNDRVIDPGKVETLTIRRLHIPRFYDLSTLYSLTERVKRITVENSKVFLVPCL  
LSQHLKSLEYLDLSENLMVEEYLKNSACEDAWPSLQTLILRQNHLASLEKTGETLLTLK  
NLTNIDISKNSFHSMPPETCQWPEKMKYLNLSSTRIHSVTGCIPKTLIELDVSNNNLNF  
SLNLPQLKELYISRNKLMTPDASLLPMLLVLKISRNAITTFSKEQLDSFHTLKTL  
GNNFICSCEFLSFTQQALAKVLIDWPANYLCDSPSHVRGQQVQDVRLSVSECHRTAL  
VSGMCCALFLLILLTGVLCHRFHGLWYMKMMWAWLQAKRKPRKAPSRNICYDAFVSYSE  
RDAYWVENLMVQELENFNPPFKLCLHKRDFIPGKWIIDNIIDSIEKSHKTVFVLSENFV  
KSEWCKYELDFSHFRLFDENNDAAILILLEPIEKKAIPQRFCRKIMNTKTYLEWPMD  
EAQREGFWVNLRRAAIKS

**FIG. 11**

## REPLACEMENT SHEET

(SEQ ID NO: 1)

Met Arg Leu Ile Arg Asn Ile Tyr Ile Phe Cys Ser Ile Val Met Thr Ala Glu Gly Asp Ala Pro Glu Leu Pro Glu Glu Arg Glu Leu	15	20	25	30
5				
Met Thr Asn Cys Ser Asn Met Ser Leu Arg Lys Val Pro Ala Asp Leu Thr Pro Ala Thr Thr Leu Asp Leu Ser Tyr Asn Leu Leu	45	50	55	60
35				
Phe Gln Leu Gln Ser Ser Asp Phe His Ser Val Ser Lys Leu Arg Val Leu Ile Leu Cys His Asn Arg Ile Gln Gln Leu Asp Leu Lys	75	80	85	90
65				
Thr Phe Glu Phe Asn Lys Glu Leu Arg Tyr Leu Asp Leu Ser Asn Arg Leu Lys Ser Val Thr Trp Tyr Leu Leu Ala Gly Leu Arg	100	105	110	115
95				
Tyr Leu Asp Leu Ser Phe Asn Asp Phe Asp Thr Met Pro Ile Cys Glu Ala Gly Asn Met Ser His Leu Glu Ile Leu Gly Leu Ser	125	130	135	140
125				
Gly Ala Lys Ile Gln Lys Ser Asp Phe Gln Lys Ile Ala His Leu Asn Thr Val Phe Leu Gly Phe Arg Thr Leu Pro His Tyr	155	160	165	170
155				
Glu Glu Gly Ser Leu Pro Ile Leu Asn Thr Thr Lys Leu His Ile Val Leu Bro Met Asp Thr Asn Phe Trp Val Leu Arg Asp Gly	185	190	195	200
185				
Ile Lys Thr Ser Lys Ile Leu Glu Met Thr Asn Ile Asp Gly Lys Ser Gln Phe Val Ser Tyr Glu Met Gln Arg Asn Leu Ser Leu Glu	215	220	225	230
215				
Asn Ala Lys Thr Ser Val Leu Leu Asn Lys Val Asp Leu Trp Asp Asp Leu Phe Leu Ile Leu Gln Phe Val Trp His Thr Ser	245	250	255	260

**FIG. 12A**

## REPLACEMENT SHEET

Val Glu His Phe Gln Ile Arg Asn Val Thr Phe Gly Gly Lys Ala Tyr Leu Asp His Asn Ser Phe Asp Tyr Ser Asn Thr Val Met Arg  
275 280 285 290 295 300

Thr Ile Lys Leu Glu His Val His Phe Arg Val Phe Tyr Ile Gln Gln Asp Lys Ile Tyr Leu Leu Thr Lys Met Asp Ile Glu Asn  
305 310 315 320 325 330

Ieu Thr Ile Ser Asn Ala Gln Met Pro His Met Leu Phe Pro Asn Tyr Pro Thr Lys Phe Gln Tyr Leu Asn Phe Ala Asn Asn Ile Leu  
335 340 345 350 355 360

Thr Asp Glu Leu Phe Lys Arg Thr Ile Gln Leu Pro His Leu Lys Thr Leu Ile Leu Asn Gly Asn Lys Leu Glu Thr Leu Ser Leu Val  
365 370 375 380 385 390

Ser Cys Phe Ala Asn Asn Thr Pro Leu Glu His Leu Asp Leu Ser Gln Asn Leu Leu Gln His Lys Asn Asp Glu Asn Cys Ser Trp Pro  
395 400 405 410 415 420

Glu Thr Val Val Asn Met Asn Leu Ser Tyr Asn Lys Leu Ser Asp Ser Val Phe Arg Cys Leu Pro Lys Ser Ile Gln Ile Leu Asp Leu  
425 430 435 440 445 450

Asn Asn Asn Gln Ile Gln Thr Val Pro Lys Glu Thr Ile His Leu Met Ala Leu Arg Glu Leu Asn Ile Ala Phe Asn Phe Leu Thr Asp  
455 460 465 470 475 480

Leu Pro Gly Cys Ser His Phe Ser Arg Leu Ser Val Leu Asn Ile Glu Met Asn Phe Ile Leu Ser Pro Ser Leu Asp Phe Val Gln Ser  
485 490 495 500 505 510

Cys Gln Glu Val Lys Thr Leu Asn Ala Gly Arg Asn Pro Phe Arg Cys Thr Cys Glu Leu Lys Asn Phe Ile Gln Leu Glu Thr Tyr Ser  
515 520 525 530 535 540

**FIG. 12B**

## REPLACEMENT SHEET

Glu Val Met Met Val Gly Trp Ser Asp Ser Tyr Thr Cys Glu Tyr Pro Leu Asn Leu Arg Gly Thr Arg Leu Lys Asp Val His Leu His  
545 555 560 565 570

Glu Leu Ser Cys Asn Thr Ala Leu Ile Val Thr Ile Val Ile Met Leu Val Gly Leu Ala Val Ala Phe Cys Cys Leu His  
575 580 585 590 595 600

Phe Asp Leu Pro Trp Tyr Leu Arg Met Leu Gly Gln Cys Thr Gln Thr Trp His Arg Val Arg Lys Thr Thr Gln Glu Gln Leu Lys Arg  
605 610 615 620 625 630

Asn Val Arg Phe His Ala Phe Ile Ser Tyr Ser Glu His Asp Ser Leu Trp Val Lys Asn Glu Leu Ile Pro Asn Leu Glu Lys Glu Asp  
635 640 645 650 655 660

Gly Ser Ile Leu Ile Cys Leu Tyr Glu Ser Tyr Phe Asp Pro Gly Lys Ser Ile Ser Glu Asn Ile Val Ser Phe Ile Glu Lys Ser Tyr  
665 670 675 680 685 690

Lys Ser Ile Phe Val Leu Ser Pro Asn Phe Val Gln Asn Glu Trp Cys His Tyr Glu Phe Tyr Phe Ala His Asn Leu Phe His Glu  
695 700 705 710 715 720

Asn Ser Asp His Ile Ile Leu Ile Leu Glu Pro Ile Pro Phe Tyr Cys Ile Pro Thr Arg Tyr His Lys Leu Lys Ala Leu Leu Glu  
725 730 735 740 745 750

Lys Lys Ala Tyr Leu Glu Trp Pro Lys Asp Arg Arg Lys Cys Gly Leu Phe Trp Ala Asn Leu Arg Ala Ala Ile Asn Val Asn Val Leu  
755 760 765 770 775 780

Ala Thr Arg Glu Met Tyr Glu Ile Gln Thr Phe Thr Glu Leu Asn Glu Glu Ser Arg Gly Ser Thr Ile Ser Leu Met Arg Thr Asp Cys  
785 790 795 800 805 810

Leu  
811

**FIG. 12C**

# REPLACEMENT SHEET

(SEQ ID No. 2)

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GAATCATCCA CGCACCTGCA GCTCTGGTGA GAGACTGCAA GCGGTGGGG TTTTGAGCTA ATCTTCATCA TTCTATGAG GAAATAAGTG GTAAAATCCCT 100
<MET (trans=1-s, dir=f, res+1)>
TGGAAATACA ATGAGACTCA TCAGAAACAT TTACATATT TGAGTATTG TTATGACAGC AGAGGGTGT GCTCCAGAGC TGCAGAAGA AAGGGAACTG 200
ATGACCAACT GCTCCAACAT GTCTCTAAGA HAGGTCCCC CAGACTGAC CCCAGGCCACA ACGACACTGG ATTATCCCTA TAACCTCCCT TTTCAACTCC 300
AGAGTTCAAGA TTTTCATTC GTCCTAACAC TGAGAGTTT GATTCTATGC CATAACAGAA TTCAACAGCT GGATCTCAA ACCTTGAAT TCAACAAGGA 400
GTTAAGATTT TAGATTTGT CTAAATAACAG ACTGAAGAGT GTAACTTGTT ATTACTGGC AGGTCTAGG TATTAGATC TTTCCTTTAA TGACTTTGAC 500
ACCATGCCDA TCTGTGAGGA AGCTGGCAAC ATGTCAACACC TGGAAATCCCT AGGTTTGAGT GGGGAAAAA TACAAAAAATC AGATTTCCAG AAAATTGCTC 600
ATCTGCACTT AAATACGTGTC TTCTTAGGAT TCAGAACTCT TCCTCATTAT GAAGAAGGTA GCCTGCCAT CTAAACACAA ACAAAACTGC ACATTTGTTT 700
ACCAATGGAC ACAAAATTCT GGGTTCTTT GCGTGTGGA ATCAAGACTT CAAAATATT AGAAATGACA AAATAGATG GCAAAGCCA ATTGTAAGT 800
TATGAAATGGC AACGAAATCT TAGTTTAGAA AATGCTAAGA CATGGTCTATT AAAGTTGATT TACTCTGGG CGACCTTTT CCTATCTTAC 900
AATTGTTTG GCATACATCA GTGGAACACT TTCAAGATCCG AAATGTGACT TTGGTGTGTA AGGCTTATCT TGACCAAT TCATTTGACT ACTCAAATAC 1000
TGTAATGAGA ACTATAAAAT TGGAGCATGT ACATTGAGA GTGTTTACA TTCAACAGGA TAAAATCTAT TTGCTTTGGA CCAAATGG CATAGAAAAC 1100
CTGACAATAT CAAATGACA ATGCCAACAC ATGCTTTCC CGAATTATCC TAGGAAATT CCATATTAA ATTGCCAA TAATATCTTA ACAGACGAGT 1200
TGTTAAAAG AACTATCCAA CTGCTCACT TGGAAACTCT CATTGAAAT GGOAAATAAC TGGAGACACT TTCTTTAGTA AGTTGCTTTG CTAAACAC 1300
ACCCCTGGAA CACTGGATC TGAGTCAAA TCTTATTACAA CATAAAATG ATGAAATG CTCAATGGCA GAAACTGGG TCAATATGAA TCTGTCATAC 1400
AATAAAATTGT CTGATTCTGT CTICAGGTGC TTGCCCAAAA GTATTCAAT ACTTGACCTA AATAATAACC AAATCCAAC TGTAACCTAA GAGACTATTC 1500
ATCTGATGGC CTTACGAGAA CTTAAATATTG CATTAAATT TCTAACTGAT CTCCTGGAT GCAGTCATT CAGTAGACTT TCAGTTCTGA ACATTGAAAT 1600
GAACTTCATT CTCAGCCCCAT CTCTGGATT TGTCAGAGC TGCCAGGAAG TTAAAACCT AAATGCCAT TCCGGTGTAC CTGTGAATTA 1700
AAAAAATTCA TTCAGCTTGA AACATATTCA GAGGTCTGTA TGCTAGATTCA TACACCTGTG AATAACCTTT AACCTAAGG GGAACCTAGGT 1800

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**FIG. 13A**

REPLACEMENT SHEET

TAAAARGACGT TCATCTCCAC GAATTATCIT GCAACACAGC TCTGTTGATT GTCAACCATTG TGGTTTATTAT GCTAGTTCTG GGGTTGGCTG TGGCCRTCTG 1900  
 CTGTCCTCCAC TTGATCTGC CCTGGTATCT CAGGATGCTA GGTCAATGCA CACAACATG GCACAGGGTT AGGAAAAACAA CCCAAGAACAA ACTCAAGAGA 2000  
 AATGTCGGAT TCCAGGATT TATTCTAC AGTGAACATG ATTCTCTG TG 97GAAGAAT GAATTGATCC CCAATCTAGA GAAGGAAGAT GTTCTATCT 2100  
 TGATTTGCCT TTATGAAAGC TACTTGACC CTGGCAAAG CATTAGTGA AATATTGTA GCITCATTGAA GAAAAGCTT AAGTCATCT TTGTTTTGTC 2200  
 TCCCACACTT GTCCAGATG AGTCCAGATC TTATGAAATT TACTTGGCC ACCACAATCT CTTCCATGAA AATTCATCT GCCTCAAGATC ATATAATTCT TATCTTACTG 2300  
 GAACCCATTIC CATTCTATG CATTCCACC AGGTATCATIA AACTGAAAGC TCTCTGGAA AAAAAGCAT ACTTGGAAATG GCCCAAGGAT AGGGTAAT 2400  
 GTGGGCTTTT CTGGCAAC CTTGAGCTG CTCTGATGAG ACAGATTG CTA **TAA** AATC CCACAGTCCT TGGGAAGTT GGGACCACT ACACCTGTTGG GATGTACATT 2600  
 GTCTCGAGGT TCTACAATCT CTCTGATGAG TAAATGTTA TAATGTTA GCAACAGAG AAATGTATGA ACTGAGACA TICACAGAGT TAATGAAGA 2500  
 GATAACAACCT TTATGAGGC ATTTCACAA TATTTTATAA AATAAAAAAT GCTTATTCCC TTCATATCAG TTTCTAGAAG GATTCTAAAG ATATGATTCCT 2700  
 ATAGAAACAC CTTCACAGT TTATAAGGGC TTATGAAAAA AGGTGTTCAT CCCCAGGATTG TTATAATCA TGAAAATGTT GGCAAGGTGC AGTGGCTCAC 2800  
 TCTTGTAACTC CCAGGCATAT GGGAGCCAA GGTGGGTGAC CCACGGGGTC AAGGAGATGG GACCATCCTG GCCAACATGG TGAAACCTTG TCTCTACTAA 2900  
 AAATACAAA ATTAGCTGGG CGTGTGTTG CACGCCTGTA GTCCCCAGCTA CTTGGGAGGC TGAGGCAGGA GAATCGCTTG AACCCGGGAG GTGGCAGTGTG 3000  
 CAGTGAGCTG AGATCGAGCC ACTGGACTCC AGCCTGGTA CAGAGCGAGA CTCCATCTCA AAAAAGAA AAAAAGAA AAAAAGAA AAAAAGATG GAAAACATCC 3100  
 TCATGCCAC AAAATAAGGT CTAATTCAAT AAATTATAGT ACATTAAATGT AATATAATAT TACATGCCAC TAAAAGAAT AAGGTAGCTG TATATTCTCT 3200  
 GGTATGGAA AACATATTA ATAATGTTATA AACATTAGG TTGGTCAAA ACTAATTGTG GTTTTGCCA TTGAATGGC ATTGAATAA AAGTGTAAAG 3300  
 AAATCTATAC CAGATGTTAGT AACATTAGG TTGGTCAAA ACTAATTGTG GTTTTGCCA TTGAATGGC ATTGAATAA AAGTGTAAAG 3400  
 TTTAGAATGA ATCTGTATTI CTTCTATAAG TAGAAAAAA ATAAAGATAG TTTTACAGC CT 3462

**FIG. 13B**